



#7

# SEQUENCE LISTING

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The Government of the United States of America  
as represented by The Secretary of the  
Department of Health and Human Services

<120> Methods of Diagnosing Multidrug Resistant Tuberculosis

<130> 015280-413100US

<140> US 09/888,320

<141> 2001-06-22

<150> US 60/214,187

<151> 2000-06-26

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 1867

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> wild-type EtaA monooxygenase (Rv3854c, EthA)

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<221> CDS

<222> (201)..(1670)

<223> EtaA

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ccggacggcc gcgcggtgcg ccggccccta ggcagcgaag cctgactggc cgcgagggtg 120

gtcaccctgg cagcttacta cgtgtcgata gtgtcgacat ctcgttgacg gcctcgacat 180

tacgttgata gcgtggatcc atg acc gag cac ctc gac gtt gtc atc gtg ggc 233

Met Thr Glu His Leu Asp Val Val Ile Val Gly

1

5

10

gct gga atc tcc ggt gtc agc gcg gcc tgg cac ctg cag gac cgt tgc 281

Ala Gly Ile Ser Gly Val Ser Ala Ala Trp His Leu Gln Asp Arg Cys

15

20

25

ccg acc aag agc tac gcc atc ctg gaa aag cgg gaa tcc atg ggc ggc 329

Pro Thr Lys Ser Tyr Ala Ile Leu Glu Lys Arg Glu Ser Met Gly Gly

30

35

40

acc tgg gat ttg ttc cgt tat ccc gga att cgc tcc gac tcc gac atg 377

Thr Trp Asp Leu Phe Arg Tyr Pro Gly Ile Arg Ser Asp Ser Asp Met

45

50

55

tac acg cta ggt ttc cga ttc cgt ccc tgg acc gga cgg cag gcg atc	425
Tyr Thr Leu Gly Phe Arg Phe Arg Pro Trp Thr Gly Arg Gln Ala Ile	
60 65 70 75	
gcc gac ggc aag ccc atc ctc gag tac gtc aag agc acc gcg gcc atg	473
Ala Asp Gly Lys Pro Ile Leu Glu Tyr Val Lys Ser Thr Ala Ala Met	
80 85 90	
tat gga atc gac agg cat atc cgg ttc cac cac aag gtg atc agt gcc	521
Tyr Gly Ile Asp Arg His Ile Arg Phe His His Lys Val Ile Ser Ala	
95 100 105	
gat tgg tcg acc gcg gaa aac cgc tgg acc gtt cac atc caa agc cac	569
Asp Trp Ser Thr Ala Glu Asn Arg Trp Thr Val His Ile Gln Ser His	
110 115 120	
ggc acg ctc agc gcc ctc acc tgc gaa ttc ctc ttt ctg tgc agc gcc	617
Gly Thr Leu Ser Ala Leu Thr Cys Glu Phe Leu Phe Leu Cys Ser Gly	
125 130 135	
tac tac aac tac gac gag ggc tac tcg ccg aga ttc gcc gcc tcg gag	665
Tyr Tyr Asn Tyr Asp Glu Gly Tyr Ser Pro Arg Phe Ala Gly Ser Glu	
140 145 150 155	
gat ttc gtc ggg ccg atc atc cat ccg cag cac tgg ccc gag gac ctc	713
Asp Phe Val Gly Pro Ile Ile His Pro Gln His Trp Pro Glu Asp Leu	
160 165 170	
gac tac gac gct aag aac atc gtc gtg atc ggc agt ggc gca acg gcg	761
Asp Tyr Asp Ala Lys Asn Ile Val Val Ile Gly Ser Gly Ala Thr Ala	
175 180 185	
gtc acg ctc gtg ccg gcg ctg gcg gac tcg ggc gcc aag cac gtc acg	809
Val Thr Leu Val Pro Ala Leu Ala Asp Ser Gly Ala Lys His Val Thr	
190 195 200	
atg ctg cag cgc tca ccc acc tac atc gtg tcg cag cca gac cgg gac	857
Met Leu Gln Arg Ser Pro Thr Tyr Ile Val Ser Gln Pro Asp Arg Asp	
205 210 215	
ggc atc gcc gag aag ctc aac cgc tgg ctg ccg gag acc atg gcc tac	905
Gly Ile Ala Glu Lys Leu Asn Arg Trp Leu Pro Glu Thr Met Ala Tyr	
220 225 230 235	
acc gcg gta cgg tgg aag aac gtg ctg cgc cag gcg gcc gtg tac agc	953
Thr Ala Val Arg Trp Lys Asn Val Leu Arg Gln Ala Ala Val Tyr Ser	
240 245 250	
gcc tgc cag aag tgg cca cgg cgc atg cgg aag atg ttc ctg agc ctg	1001
Ala Cys Gln Lys Trp Pro Arg Arg Met Arg Lys Met Phe Leu Ser Leu	
255 260 265	
atc cag cgc cag cta ccc gag ggg tac gac gtg cga aag cac ttc gcc	1049
Ile Gln Arg Gln Leu Pro Glu Gly Tyr Asp Val Arg Lys His Phe Gly	
270 275 280	
ccg cac tac aac ccc tgg gac cag cga ttg tgc ttg gtg ccc aac gcc	1097
Pro His Tyr Asn Pro Trp Asp Gln Arg Leu Cys Leu Val Pro Asn Gly	
285 290 295	

gac ctg ttc cgg gcc att cgt cac ggg aag gtc gag gtg gtg acc gac	1145
Asp Leu Phe Arg Ala Ile Arg His Gly Lys Val Glu Val Val Thr Asp	
300 305 310 315	
acc att gaa cgg ttc acc gcg acc gga atc cgg ctg aac tca ggt cgc	1193
Thr Ile Glu Arg Phe Thr Ala Thr Gly Ile Arg Leu Asn Ser Gly Arg	
320 325 330	
gaa ctg ccg gct gac atc atc att acc gca acg ggg ttg aac ctg cag	1241
Glu Leu Pro Ala Asp Ile Ile Ile Thr Ala Thr Gly Leu Asn Leu Gln	
335 340 345	
ctt ttt ggt ggg gcg acg gcg act atc gac gga caa caa gtg gac atc	1289
Leu Phe Gly Gly Ala Thr Ala Thr Ile Asp Gly Gln Gln Val Asp Ile	
350 355 360	
acc acg acg atg gcc tac aag ggc atg atg ctt tcc ggc atc ccc aac	1337
Thr Thr Thr Met Ala Tyr Lys Gly Met Met Leu Ser Gly Ile Pro Asn	
365 370 375	
atg gcc tac acg gtt ggc tac acc aat gcc tcc tgg acg ctg aag gcc	1385
Met Ala Tyr Thr Val Gly Tyr Thr Asn Ala Ser Trp Thr Leu Lys Ala	
380 385 390 395	
gac ctg gtg tcg gag ttt gtc tgt cgc ttg ttg aat tac atg gac gac	1433
Asp Leu Val Ser Glu Phe Val Cys Arg Leu Leu Asn Tyr Met Asp Asp	
400 405 410	
aac ggt ttt gac acc gtg gtc gtc gag cga ccg ggc tca gat gtc gaa	1481
Asn Gly Phe Asp Thr Val Val Val Glu Arg Pro Gly Ser Asp Val Glu	
415 420 425	
gag cgg ccc ttc atg gag ttc acc cca ggt tac gtg ctg cgc tcg ctg	1529
Glu Arg Pro Phe Met Glu Phe Thr Pro Gly Tyr Val Leu Arg Ser Leu	
430 435 440	
gac gag ctg ccc aag cag ggt tcg cgt aca ccg tgg cgc ctg aat cag	1577
Asp Glu Leu Pro Lys Gln Gly Ser Arg Thr Pro Trp Arg Leu Asn Gln	
445 450 455	
aac tac cta cgt gac atc cgg ctc atc cgg cgc ggc aag atc gac gac	1625
Asn Tyr Leu Arg Asp Ile Arg Leu Ile Arg Arg Gly Lys Ile Asp Asp	
460 465 470 475	
gag ggt ctg cgg ttc gcc aaa agg cct gcc ccg gtg ggg gtt tag	1670
Glu Gly Leu Arg Phe Ala Lys Arg Pro Ala Pro Val Gly Val	
480 485 490	
ctttagcgac ggttttagcgc cggtttaggc catagtcaga cgacgatgat gccgtcgtcg	1730
tcgctgtagg cgatatcgcc cggaacgaat gtcaccccgcc ccagcgtgat ttcaacgtcg	1790
cgttctccgg caccggtctt ggtgctcttg cggggattgg tgcccagcgc tttgatgccg	1850
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 <212> PRT  
 <213> Mycobacterium tuberculosis  
 <223> wild-type EtaA monooxygenase (Rv3854c, EthA)

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 35 40 45  
 Arg Tyr Pro Gly Ile Arg Ser Asp Ser Asp Met Tyr Thr Leu Gly Phe  
 50 55 60  
 Arg Phe Arg Pro Trp Thr Gly Arg Gln Ala Ile Ala Asp Gly Lys Pro  
 65 70 75 80  
 Ile Leu Glu Tyr Val Lys Ser Thr Ala Ala Met Tyr Gly Ile Asp Arg  
 85 90 95  
 His Ile Arg Phe His His Lys Val Ile Ser Ala Asp Trp Ser Thr Ala  
 100 105 110  
 Glu Asn Arg Trp Thr Val His Ile Gln Ser His Gly Thr Leu Ser Ala  
 115 120 125  
 Leu Thr Cys Glu Phe Leu Phe Leu Cys Ser Gly Tyr Tyr Asn Tyr Asp  
 130 135 140  
 Glu Gly Tyr Ser Pro Arg Phe Ala Gly Ser Glu Asp Phe Val Gly Pro  
 145 150 155 160  
 Ile Ile His Pro Gln His Trp Pro Glu Asp Leu Asp Tyr Asp Ala Lys  
 165 170 175  
 Asn Ile Val Val Ile Gly Ser Gly Ala Thr Ala Val Thr Leu Val Pro  
 180 185 190  
 Ala Leu Ala Asp Ser Gly Ala Lys His Val Thr Met Leu Gln Arg Ser  
 195 200 205  
 Pro Thr Tyr Ile Val Ser Gln Pro Asp Arg Asp Gly Ile Ala Glu Lys  
 210 215 220  
 Leu Asn Arg Trp Leu Pro Glu Thr Met Ala Tyr Thr Ala Val Arg Trp  
 225 230 235 240  
 Lys Asn Val Leu Arg Gln Ala Ala Val Tyr Ser Ala Cys Gln Lys Trp  
 245 250 255  
 Pro Arg Arg Met Arg Lys Met Phe Leu Ser Leu Ile Gln Arg Gln Leu  
 260 265 270  
 Pro Glu Gly Tyr Asp Val Arg Lys His Phe Gly Pro His Tyr Asn Pro  
 275 280 285  
 Trp Asp Gln Arg Leu Cys Leu Val Pro Asn Gly Asp Leu Phe Arg Ala  
 290 295 300  
 Ile Arg His Gly Lys Val Glu Val Val Thr Asp Thr Ile Glu Arg Phe  
 305 310 315 320  
 Thr Ala Thr Gly Ile Arg Leu Asn Ser Gly Arg Glu Leu Pro Ala Asp  
 325 330 335  
 Ile Ile Ile Thr Ala Thr Gly Leu Asn Leu Gln Leu Phe Gly Gly Ala  
 340 345 350  
 Thr Ala Thr Ile Asp Gly Gln Gln Val Asp Ile Thr Thr Met Ala  
 355 360 365  
 Tyr Lys Gly Met Met Leu Ser Gly Ile Pro Asn Met Ala Tyr Thr Val  
 370 375 380  
 Gly Tyr Thr Asn Ala Ser Trp Thr Leu Lys Ala Asp Leu Val Ser Glu  
 385 390 395 400  
 Phe Val Cys Arg Leu Leu Asn Tyr Met Asp Asp Asn Gly Phe Asp Thr  
 405 410 415  
 Val Val Val Glu Arg Pro Gly Ser Asp Val Glu Glu Arg Pro Phe Met  
 420 425 430

Glu Phe Thr .Pro Gly Tyr Val Leu Arg Ser Leu Asp Glu Leu Pro Lys  
           435                                  440                  445  
 Gln Gly Ser Arg Thr Pro Trp Arg Leu Asn Gln Asn Tyr Leu Arg Asp  
           450                                  455                  460  
 Ile Arg Leu Ile Arg Arg Gly Lys Ile Asp Asp Glu Gly Leu Arg Phe  
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 Ala Lys Arg Pro Ala Pro Val Gly Val  
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 <213> Artificial Sequence

<220>  
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           amplification primer

<400> 3  
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<210> 4  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

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<210> 5  
 <211> 18  
 <212> DNA  
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<220>  
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           sequencing primer, EtaA amplification primer

<400> 5  
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<210> 6  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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           sequencing primer, EtaA amplification primer

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 aagctgcagg ttcaacc

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<210> 7  
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<213> Artificial Sequence

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sequencing primer, EtaA amplification primer

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sequencing primer, EtaA amplification primer

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sequencing primer, EtaA amplification primer

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:EtaA Primer 3  
sequencing primer, EtaA amplification primer

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sequencing primer, EtaA amplification primer

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sequencing primer, EtaA amplification primer

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17

<210> 13  
<211> 17  
<212> DNA  
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<220>  
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sequencing primer, EtaA amplification primer

<400> 13  
tctatttccc atccaag

17

<210> 14  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:EtaA Primer 3  
sequencing primer, EtaA amplification primer

<400> 14  
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<210> 15  
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<212> DNA  
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amplification primer

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<210> 16  
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<223> Description of Artificial Sequence:EtaR PCR  
amplification primer

<400> 16

ataagaatgc ggccgcgcgg ttctcgccgt aaatgct

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